SECTEMBER LISTING

<110> JENTSCH, Thomas J. <120> NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS <130> 2815-127P <1140 h <141> <:160> 41 <100 FatentIn Ver. 2.1</pre> -:0100-1 +:211:- 2335 HIDIZH INA +:213. Homo sapiens -1220 --:2011 - gene +(2211+-1)..(2335)-1.120n --2211 - CDS H2222 - .33)..(2170) <400 - 3 agocathogt etetgagogo deegagogog deedegeede ggadogtgoo egggeedegg 60 egoescage coggegoege de atg geo gag geo des eeg ego eta gge 112 Met Ala Glu Ala Pro Pro Arg Arg Leu Gly 10 160 sty ygt dec seg dec ggg gad god dec ogd geg gag eta gtg geg etc Lei Sly Pro Pro Pro Gly Asp Ala Pro Arg Ala Glu Leu Val Ala Leu 1.5 20 and don dtd had ago day cad ddo day ddo ddo ddo cod Thr Ala Val Gln Ser Glu Gln Gly Glu Ala Gly Gly Gly Ser Pro 40 3.) 35 egologo ete ggoloto etg ggolago ees etg eeg eeg ggolgeg ees eta - 256 Arg Arg Leu Sly Leu Leu Gly Ser Pro Leu Pro Pro Sly Ala Pro Leu 50 55

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gcc Ala 75	gog Ala	cac His	aag Lys	ogo Arg	tac Tyr 30	aga Arq	ege Arg	atg Leu	cag Gln	aac Asn 85	tgg Trp	gtc Val	tac Tyr	aac Asn	gtg Val 90	352
ctg Leu	gag Glu	ogg Arg	ado Pro	age Arg 95	ggc Gly	tgg Trp	gee Ala	tta Phe	gtc Val 100	tac Tyr	cac His	gtc Val	tto Phe	ata Ile 105	ttt Phe	400
ttg Leu	ctg Leu	gtc Val	tic Pne	agc Ser	tgc Cys	ctg Leu	gtg Val	ctg Leu 115	tot Ser	gtg Val	ctg Leu	taa Ser	act Thr 120	atc Ile	cag Gln	448
gag Glu	cac His	cag Gln 125	gaa Glu	ctt Leu	gcc Ala	aac Asn	gag Glu 130	tgt Cys	ata Leu	ctc Leu	atc Ile	ttg Leu 135	gaa Glu	ttc Phe	gtg Val	496
atg Met	atc Ile 140	gtg Val	gtt Val	ttc Phe	ggc Gly	ttg Leu 145	Glu	tac Tyr	atc Ile	gtc Val	cgg Arg 150	gtc Val	tgg Trp	tcc Ser	gcc Ala	544
gga Gly 155	Cys	tgc Cys	tgc Cys	cgc Arg	tac Tyr 160	Arg	gga Gly	tgg Trp	cag Gln	ggt Gly 165	Arg	ttc Phe	ege Arg	ttt Phe	gcc Ala 170	592
aga Arg	aag Lys	cee Pro	ttc Fhe	tgt Cys	Val	atc Ile	: dac : Asp	tto Phe	atc Ile 180	gtg Val	tto Phe	gtg Val	gcc Ala	tcg Ser 185	Val	640
gcc Ala	gtc Val	ato Ile	: gac : Ala : 190	a Ala	ggt Gly	acc Thr	d dag Gln	ggc Gly 195	Asn	ato i Ile	t t c	gcc Ala	acg Thr 200	Ser	gcg Ala	688
cto Lei	g ogo : Arg	: ago g 3er 205	: Met	g aga t Ara	: tto ; Phe	c otç e Lei	g dag i Slr 210	ı Ile	ctq Lev	g ogo : Arg	atg Met	gtg Val	. Arg	atg Met	gac : Asp	736
eg@ Ar@	e ogo g Arg 220	g (31)	2 gg(e acc y Thi	c tgg Trị	g aaq D Lys 225	s Lei	g atq ı Lev	g gg¢ i Glà	c tca y Ser	gtç Val 230	. Val	tac Tyr	geg Ala	g cat His	784
ago Se: 23:	r Ly:	g gaq s Gli	g ote i Lee	g ato u Ile	acc Thi	c Ala	e tgo a Trp	g tak o Tyn	at: r Ile	c ggg e Gly 248	/ Phe	c ctq e Lei	g gtq ı Val	rcto Lev	atc ille 250	832

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acc Thr	ato Tie	285 ggc	tat Tyr	ggt Gly	gac Asp	aag Lys	aca Thr 290	Pro	cac His	aca Thr	tgg Trp	atg Leu 295	ggo Gly	agg Arg	gto Val	976
ctg Leu	get Ala 300	gct Ala	ggc Gly	ttc Phe	gcc Ala	tta Leu 305	ctg Leu	ggc Gly	atc Ile	tot Ser	ttc Phe 310	ttt Phe	gcc Ala	ctg Leu	cct Pro	1024
gcc Ala 315	Gly	atc Ile	cta Leu	ggc Gly	too Ser 320	ggc Gly	ttt Phe	gos Ala	ctg Leu	aag Lys 325	gto Val	cag Gln	gag Glu	cag Gln	cac His 330	1072
cgg Arg	cag Gln	aag Lys	cac His	ttc Phe 335	Glu	aag Lys	cgg Arg	agg Arg	atg Met 340	Pro	gca Ala	gcc Ala	aac Asn	ctc Leu 345	. ile	1120
cag Gln	gct Ala	gco Ala	tgg Trp 350	Arg	ctg Leu	tac Tyr	toc Ser	acc Thr 355	gat Asp	atg Met	agc Ser	cgg Arg	gdd Ala 360	tac Tyr	: ctg - Leu	1168
aca Thr	n gee Ala	aco Thi	Tr	g tac D Tyr	: tac : Tyr	tat Tyr	gac Asp 370	Ser	ato Ile	cto Leu	c oda i Pro	tdo Ser 375	Phe	aga Arg	a gag g Glu	1216
cto	g geo 1 Ala 380	Leu	d titq i Let	g ttt 1 Phe	: gaç e Glu	g cac i His 385	: Val	g caa Gln	. ogç . Arç	g god g Ala	c aga Arg 390	ASI	gyg Gly	. GJ7	c cta / Leu	1264
cgo Aro 399	g Pro	c ct	g gad u Gli	g gtç u Val	g cgg L Arg 400	g Ard	j doč	g ddg A Pro	g gta Val	a coc l Pro 403	o Asp	o gga	rgba rAla	n ecc	s too Ser 410	1312
cg: Ar	t tad g Ty:	c cc r Pr	g cc o Pr	c gtt b Val 419	l Ala	e acc	d tgo c Oys	e cas s His	c cgc 5 Arc 42	g Pr	g gge	c ago 7 Ser	c acc	ta: Se: 42	c tto r Phe 5	1360
tg Cy	c cc s Pr	t gg o Gl	g ga y Gl 45	u Sei	c ag r Se	c cge r Are	g ato g Me	g ggG t Gly 439	y Il	сазю e Ly.	a ga- s Asi	c og: p Ar:	at: g Ila 440	e Ar	c atg g Met	1408

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occ Pro	tca Ser	gag Glu	gaa Glu 510	Val	gca Ala	gag Glu	gag Glu	aag Lys 515	agc Ser	tac Tyr	cag Gln	tgt Cys	gag Glu 520	ct.c Leu	acg Thr	1648
gtg Val	gac Asp	gac Asp 515	atc Ile	atg Met	cct Pro	gct Ala	gtg Val 530	aag Lys	aca Thr	gtc Val	atc Ile	cgc Arg 535	toc Ser	atc Ile	agg Arg	1696
Ile	Leu 540	Lys	Fhe	. Leu	Val	Ala 545	Lys	Arg	Lys	: Phe	: Lys 550	(Glu	Thr	reu		1744
cog Pro 555	tac Tyr	gac Asp	gtg Val	, aag . Lys	gac Asp 560	Val	att Ile	gag Glu	cag Glr	tac Tyr 565	Ser	gca Ala	ggc Gly	cac His	ctg Leu 570	17 92
gac Asp	atg Met	oto	ı Gly	c agg y Arg 575	g Ile	: aag : Lys	agc Ser	ctq Leu	g daa n Glr E80	n Thi	. ogg . Arg	g gtg g Val	gac Asp	caa Gln 585	1 116	1640
Val	Gly	Arq	59:	y Pro O	o Glj	y Asp	Arg	595 595	s Ala	a Aro	g Gil	n pag	600 600	/ ASP	aag Lys	1868
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i1et Asg	t Ala l p Ala	a Glu a Pro	n Ala D Arg 20	Pro E : Ala	. Glu	. Let	ı Val	Ala 25	10 Let	i 1 Thr	Ala	. Val	. Glr 30	Se	o r Gl	U
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ilet Asi	a Ala l p Ala n Gly	a Glu a Pro y Glu 3:	n Ala Arg 20 2 Ala	Pro E Ala Gly	. Glu . Gly	. Let / Gly	n Val 7 Gly 40	Ala 25 Y Ser	10 Let Pro	Thr Arç	r Ala g Arg	Val Leu 45	Glr 30 1 Gly	Se Le	r Gl u Le	u u
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Met As: Gl:	n Ala y Ala y Se	a Glu a Pro y Glu 3: r Pro	n Ala 20 20 2 Ala 5 5	Pro E Ala Gly	. Glu . Gly o Pro	. Let ; Gly o Gly 55	r Val / Gly 40 / Ala	Ala 25 Y Ser) a Pro	10 Let Pro	Thr Arç	Ala g Arg o Gly	Value	Glr 30 1 Gly 5 Gly	Se Le Se	r Gl u Le r Gl	u u y
idet Ass Gl: Se	Ala I n Ala y Se 5	a Glu a Pro y Glu 3: r Pro	n Ala 20 20 2 Ala 5 5	Pro E Ala Gly	Glu Gly D Pro	. Det / Gly b Gly 50 / Gly	r Val / Gly 40 / Ala	Ala 25 Y Ser) a Pro	10 Let Pro	Thr Argo Argo Pro	r Ala g Arg o Gly 60 a Ala	Value	Glr 30 1 Gly 5 Gly	Se Le Se	r Gl u Le r Gl g Ty	u u y
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Ass 31: 31: Se 6	n Ala p Ala n Ala y Se 5 r Gl 5 g Ar	a Glu a Pro y Glu 3: r Pro 0 y Se. g Le	n Ala D Arg 20 2 Ala D Lev r Ala u Gla	Pro E: Ala E: Gly E: Gly E: Cys E: Asi 8:	Glu Gly Gly Gly Gly Tri	. Det 7 Gly 55 7 Gli 9 Va	y Gly 40 Y Ala 5 n Arc	Ala 25 Y Ser O a Pro g Ser r Asi	10 Let Pro Det Det 1 Va.	Thr Arg	Ala Arg Gly 60 Ala Ala 5	Value Leu 45 Pro Pro His	Glr 30 Gly D Gly s Ly	Se Le Ar Ar	r Gl u Le r Gl g Ty 8 g Gl	u y r o y
Ass 31: 31: Se 6	n Ala p Ala n Ala y Se 5 r Gl 5 g Ar	a Glu a Pro y Glu 3: r Pro 0 y Se. g Le	n Ala 20 20 21 Ala 5 5 5 6 Lev 4 8 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Pro E Ala Gly Pro A Cys n Ass 81	Glu Gly Gly Gly Gly Tri	. Det 7 Gly 55 7 Gly 9 Va	y Gly 40 Y Ala 5 n Arc	Ala 25 Y Ser O Pro g Ser Asi	10 Let Pro Let 9 Pho	Thr Arg	Alaman Argonal Argonal Alaman	Value Leu 45 Pro Pro His	Glr 30 Gly Gly S Ly g Pr l Ph	Se Se Ar Ar Se Se	r Gl u Le r Gl g Ty 8 g Gl	u y r o y
Met As; As; Gl: Se 6 Ar	y Se 5 7 31 5 9 Ar	a Glu y Glu y Glu y Se y Se a Ph	a Ala D Arg 20 1 Ala 5 D Let T Ala U Gli e Va 10	Pro E Ala A Gly A Cys D Ass B Tys	Glu Gly Gly Gly Gly Tr Tr Tr Tr	Gly Gly Gly Gly Gly Gly Gly D Va	y Gly Alaban Architecture (1994)	Ala 25 Y Ser O Pro g Ser Asi e Ilo	10 Let Pro Let 9 Pho 5	Thr Arc	Ala y Arg O Gly 60 a Ala 5 u Ciu	Value	Glr 30 Gly 6 6 Cly S Ly: g Pr 1 Ph 11	Se Se Ar Ar Se Se	r Gl u Le r Gl g Ty 8 g Gl	u y x 0 y
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Met Ass Slu Slu Se 6 Ar Tr	y Se r Sl g Ar F Al	a Glu a Pro y Glu 33 r Pro y Se. y Se. a Ph 1 Le il	a Ala Arç 20 20 Ala 5 Lev r Ala u Gli e Va 10 u Se 5	Pro E: Ala : Ala : Gly : Pro a Cys a Cys a Cys b Asi 8! I Ty: 0	Glu Gly Pro Gly 70 Tr; 5 r Hi:	Gly Gly Gly Gly Gly Gli Va Se U Se	Y Gly 4(Y Alas	Ala 25 / Ser D a Pro g Ser r Asi e Ill 10 r Ill	10 Let Pro Let Va. 90 Pho E Gl	Thr Thr Arg	Ala Arg Arg 60 a Ala 50 u Leu u Hi:	Value	Glr 30 Gly 6 Gly 8 Ly 9 Pr 1 Ph 11 n Gl	Se Ar Se Se Se Du Le	r Gl u Le r Gl g Ty 8 g Gl 95 cr Cy	u y y o y
Met Ass Sl. Sl. Se 6 Ar Tr	y Se r Sl g Ar F Al	a Glu a Pro y Glu 33 r Pro y Se. y Se. a Ph 1 Le il	a Ala Arç 20 20 Ala 5 Lev r Ala u Gli e Va 10 u Se 5	Pro E: Ala : Ala : Gly : Pro a Cys a Cys a Cys b Asi 8! I Ty: 0	Glu Gly Pro Gly 70 Tr; 5 r Hi:	Gly Gly Gly Gly Gly Gli Va Se U Se	Y Gly 4(Y Alas	Ala 25 / Ser D a Pro g Ser r Asi e Ill 10 r Ill	10 Let Pro Let Va. 90 Pho E Gl	Thr Thr Arg	Ala Arg Arg 60 a Ala 50 u Leu u Hi:	Value	Glr 30 Gly 6 Gly 8 Ly 9 Pr 1 Ph 11 n Gl	Se Ar Se Se Se Du Le	r Gl u Le r Gl g Ty 8 g Gl 95 cr Cy	u y y o y
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Let Glu Tyr II. Val Arg Val Trp Ser Ala Gly Cys Cys Arg Tyr

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Arg	317	Trp	Jin	Giş 168	Arg	Phe	Arg	Fhe	Ala 170	Arg	<u>.</u> ;s	Fro	Fhe	Cys Ins	Val
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Thr	Gln	Gly 195		Ile	Phe	Ala	Thr 200		Ala	Leu	Arg	Ser 205	Met	Arg	Phe
Leu		Ile	Leu	Arg	Met	Va1 215		Met	Asp	Arg	Arg 220		Gly	Thr	Trp
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225					230					235					240
		Tyr		245					250					255	
Tyr	Leu	. Ala	Glu 260	Lys	Asp	Ala	Asn	Ser 265	Asp	Phe	Ser	Ser	Tyr 270	Ala	Asp
Ser	Leu	Trp 275		Gly	Thr	Ile	Th.r 280	Leu	Thr	Thr	Ile	Gl.y 285		Gly	Asp
Lys	Thr 290	Pro		Thr	Trp	Leu 295	Gly	Arg	Val.	Leu	Ala 300		Gly	Ph.e	Ala
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		e Ala	Leu	Lys 325	Val	Gln	Glu	Gln	His		Gln	Lys	His	Phe 335	
Lys	s Arç	g Arg	Met 340	Pro		Ala	Asn	Leu 345	Ile		Ala	Ala	Trp 350		Let
Туг	s Ser	Thr 355	Asp		Ser	Arg	Ala 360	Tyr		Thr	Ala	Thr 365		Tyr	Ту
Tyr	r Asp 370	ser		Leu	Pro	Jer 375	Phe		Glu	Leu	Ala 380	Leu		Phe	G.,1
His	s Val	l Gln	Arg	Ala	Arg 390	Asn		Gly	Leu	Arg 395	Pro		Glu	. Val	Ar 40
		a Pro	- Val	Pro 405	Lsp		Ala	Pro	Ser 41)	Arg		Pro	Pro	Val 415	
Thi	r Cys	s His	Arg 420	Pro		Ser	Thr	Ser 425	Phe		Pro	Gly	/ Glu 430	Ser	
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Val	V 11 610		Glu	Ile	Ser	Met 615		Gly	Arg	Val	Val 620	Lys	Val	Glu	Lys	
Gln 635		Gln	Ser	Ile	Glu 630		Lys	Leu	Asp	Leu 635		Leu	Gly	Phe	Tyr 640	
	Arg	Cys	Leu	Arg 645		Gly	Thr	Ser	Ala 650		Leu	Gly	Ala	Val 655	Gln	
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+510 + 7	
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artarigteeg egetgtgaee	20
4449coog ogoogagaaa	
- 11: - 20	
- 31 DNA	
RE1135 Artificial Sequence	
42374	
.223 Description of Artificial Sequence: PCR Primer	
Ed. Description of the end of	
4952-8	
igtotocagg gtcagagtog	20
agebookagg geomgmaken	

RETURNATION OF THE PROPERTY OF	
K2.12 + DWA	
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<220 ·	
<pre><220</pre>	
K.M.A. Bescription of Altificial Codds. 100 from	
< 400 × 9	
t ogradg tgogoggggt a	2. <u>.</u>
1:.10	
1: . 21	
12 - ENA	
·11: Artificial Sequence	
+220 +	
1723 Description of Artificial Sequence: PCR Primer	
· 400 · 10	
pagabageed etetgacete g	21
aagabagbee etetgaeete g	
- 0110 × 11	
·11. · 21	
+.111 + DNA	
13 - Artificial Sequence	
- 2007 - Description of Artificial Sequence: PCR Primer	
The second of Medical address.	
+4% + 11	21
atomotitico ogigiggaag o	2.1
+ MIR + 12	
+31 + 21	
+ DI. + PNA	
- 213 - Artificial Sequence	
+ 210 +	
2.00 · Description of Artificial Sequence: PCR Primer	
Description of Artificial Dequence. For Filmor	
400 - 12	
agtbacgatg ggcagacotc g	21

62108 DMA	
k213> Artifictal Sequence	
20 •</td <td></td>	
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< 400 ÷ 13	7, 7 7, 4
u toatgato aggotootad o	€ <u></u>
+.10 × 14	
+ 112 + ENA	
+113 - Artificial Sequence	
t	
- 000×	
-123 Description of Artificial Sequence: PCR Primer	
+400 + 14	
atgtqtgaca ggggtgagc	19
+ 010 × 15	
+ 211 + 20	
In - DNA	
-:11: Artificial Sequence	
- 2.90 ·	
: Description of Artificial Sequence: PCR Primer	
Dissipation of Management,	
+47++15	
anguatgggg acaccettge	20
16	
·.::· 13	
- DIA - DNA	
- 113 · Artificial Sequence	
- U20 -	
+ 222 + Description of Artificial Sequence: PCR Primer	
. Lar Description of Artificial Sequence. For filmer	
40∴ 16	
.pacagggtt gacacacc	18

\$2118 U1	
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K220N	
<pre></pre> <pre>Class Description of Artificial Sequence: FCR Primer</pre>	
+1 4 0 (10 + 10)	
pitorgagta acceacaact g	2.1
HC 10H 18	
HILL: 21	
-0.120-11 N A	
2130 Artificial Sequence	
Tit. Mitilitat beguenee	
-120	
CL20*	
-0.783 Description of Artificial Sequence: PCR Primer	
4400 · 16	0.1
gotobootgg gagocatoac c	21
4010 + 1 +	
on the rna	
ा. 17 - Artificial Sequence	
H1213 ·	
- PCR Primer	
H14 10 + 1 +	
	20
tyanthagg agototgtgo	20
(0.10 + 1.0)	
11111 - DUA	
-013 - Artificial Sequence	
-1.120 -	
4223 · Description of Artificial Sequence: PCR Primer	
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abobaogaag tggotgaagg c	21

*211 * 22	
S212 DW	
k213% Artificial Sequence	
<220>	
<2230 Description of Artificial Sequence: PCR Primer	
N.223% Beschiperon of Architecture Ecquence Figure 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	
gtodiaegta agattigiaa	2.0
geom angen agenergees	
49.00 22	
+:210:- 22	
S0110-20	
HILLING THA	
31120 Artificial Sequence	
+1.1.20 ·	
RING - Description of Artificial Sequence: PCR Primer	
5(400 × 2);	
potbagbogg cootogatog	20
H217 + U3	
+1211 + 20	
POST CONTRACTOR CONTRA	
HC113 - Artificial Sequence	
- Carlo Micrifolds Dequence	
ennio e	
HEARTH Description of Artificial Sequence: PCR Primer	
-440° + 23	20
sastistastg gtggtttggc	.: 0
$\sim 0.110 \times 24$	
<211 < 20	
HARAM DNA	
4.213 - Artificial Sequence	
·(22) ·	
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nthothacat caaqtqatqq	20

ctcctgacct caagtgatcc

K0108-DMA	
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K400% 29	
titgryptto poagataago	20
Ht2 1 0 (+ 3 0	
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112 - ENA	
-: 213 - Artificial Sequence	
.bit fireing objective	
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Will rescription of Mithiotal Boquesov 110 120	
<400 · 30	
	24
сдідзіў dag tgagttcaag tacg	
- MILO - 31	
*:111 + 24	
H. II - DNA	
-1.13 - Artificial Sequence	
DCB Primar	
-0003 - Description of Artificial Sequence: PCR Primer	
	24
artanotyat gyagogosot otog	27
-1.110 + 32	
H:::11 + 24	
-CIII - DNA	
-1113 - Artificial Sequence	
:223 · Description of Artificial Sequence: PCR Primer	
(4) 9 + 32	~ <i>*</i>
teatecaceg taageteaca etgg	24

9001 3 33 9011 + 606

SILLE FRI

<2135 Homo sapiens

<4000 33

Met Ala Ala Ala Ser Ser Pro Pro Arg Ala Glu Arg Lys Arg Trp Gly

Trp Sly Ard Led Pro Sly Ala Arg Arg Sly Ser Ala Sly Led Ala Lys 20 25 30

Lys Cys Prc Phe Ser Leu Glu Leu Ala Glu Gly Gly Pro Ala Gly Gly 40 45

Ala Leu Tyr Ala Pro Ile Ala Pro Gly Ala Pro Gly Pro Ala Pro Pro 50 55 60

Ala Ser Pro Ala Ala Pro Ala Ala Pro Pro Val Ala Ser Asp Leu Gly 65 70 75 80

Pro Arg Pro Pro Val Ser Leu Asp Pro Arg Val Ser Ile Tyr Ser Thr 85 90 95

Arg Arg Pro Val Leu Ala Arg Thr His Val Gln Gly Arg Val Tyr Asn 100 105 110

Phe Leu Glu Arg Pro Thr Gly Trp Lys Cys Phe Val Tyr His Phe Ala 115 $$120\$

Val Phe Leu Ile Val Leu Val Cys Leu Ile Phe Ser Val Leu Ser Thr 130 135 140

Ile Val Leu Val Val Phe Phe Gly Thr Glu Tyr Val Val Arg Leu Trp 165 170 175

Ser Ala Gly Cys Arg Ser Lys Tyr Val Gly Leu Trp Gly Arg Leu Arg 180 185

Phe Ala Arg Lys Pro Ile Ser Ile Ile Asp Leu Ile Val Val Val Ala 195 200 205

Ser Met Val Val Leu Cys Val Gly Ser Lys Gly Gln Val Phe Ala Thr 210 215 220

Ser Lis	A 1 :	Tie	Arg		ile . 330	Arş	i he	Les	311.	11.0 235	lista i	AIJ :	Net.		::1 <i>5</i> 2 4 .
Val	Asp	Arg		Gly 245	Gly	Thr	Trp		Leu 250	Leu	Gly	Ser	Val	Val 255	Phe
Ile	His	Arg	Gln 260	Glu	Leu	:le	Thr	Thr 265	Leu	Tyr	Ile	Gly	Phe 270	Leu	Gly
Leu	11.6	Phe 275	Ser	Ser	Tyr	Phe	Val 280	Tyr	Leu	Ala	Glu	1ys 295	Asp	Ala	Val
Asn	Glu 290		Glγ	Arg	Val	Glu 295	Phe	Gly	Ser	Tyr	Ala 300	Asp	Ala	Leu	Trp
Trp 305		Val	Val	Thr	Val	Thr	Thr	Ile	Gly	Tyr 315	Gly	qzA	Lys	Val	Pro 320
Gln	. Thr	Trp	Val	Gly 325		Thr	Ile	Ala	Ser 330	Cys	Phe	Ser	Val	Phe 335	Ala
Ile	e Ser	Phe	Phe		Leu	Pro	Ala	Gly 345		Leu	Gly	Ser	Gly 350	Phe	Ala
Leu	i Lys	355		Gln	Lys	Gln	Arg 360		Lys	His	Phe	Asn 365	Arg	Gln	Ile
Pro	370		a Ala	s Ser	: Leu	. Ile 375		Th.r	Ala	a Trp	Arg 380	Cys	Tyr	Ala	Ala
Gl: 38:		n Pro	o Asp	Ser	Ser 390		Trp	> Lys	; Il∈	∍ Tyr 395	: Ile	e Arg	Lys	Ala	Pro 400
Ar	g Se:	r Hi:	s Thi	c Let 405		ı Ser	Pro	ser	Pro 410	o Lys	s Pro	Lys	. Lys	Ser 415	· Val
Va	l Va.	l Ly	s Ly:		s Lys	s Phe	e Lys	s Let 425		p Lys	s Asp	Asr	n Gly 430	y Val	. Thr
Pr	o Gl	y Gl 43		s Me	t Lei	ı Thi	r Val		o Hi	s Ile	e Tho	c Cys 445	s Asp	o Pro) Pro
Gl	u 31 45		g Ar	g Le	u Asp	p Hi: 45.		e Se	r Va	l As	p Gly 463		r Asņ	o Sei	s Ser

Val Arq Lys Ser Pro Thr Leu Leu Glu Val Ser Met Pro His Phe Met 465 470 475 480

Ar: The Ash Ser Ene Ala (1): Asy Lea Asp Lea Gla Gla Gla Thr Lea 485 491 491

Leu Thr Pro Ile Thr His Ile Ser 31n Leu Arg Glu His His Arg Ala 500 505 510

Thr Ile Lys Val Ile Arg Arg Met Gln Tyr Phe Val Ala Lys Lys 515 526

Phe Gln Gln Ala Arg Lys Pro Tyr Asp Val Arg Asp Val Ile Glu Gln 530 535 540

Tyr Ser Gln Gly His Leu Asn Leu Met Val Arg Ile Lys Glu Leu Gln 545 550 550 560

Arg Arg Leu Asp Gln Ser Ile Gly Lys Pro Ser Leu Phe Ile Ser Val 565 570 575

Ser Glu Lys Ser Lys Asp Arg Gly Ser Asn Thr Ile Gly Ala Arg Leu 580 585 590

Asn Arg Val Glu Asp Lys Val Thr Gln Leu Asp Gln Arg Leu Ala Leu 595 600 605

lle Thr Asp Met Leu His Gln Leu Leu Ser Leu His Gly Gly Ser Thr 610 620

Fro Gly Ser Gly Gly Pro Pro Arg Glu Gly Gly Ala His Ile Thr Gln $\mathfrak{C}25$ 630 635 640

Fro Cys Gly Ser Gly Gly Ser Val Asp Pro Glu Leu Phe Leu Pro Ser 645 650 655

Asn Thr Leu Pro Thr Tyr Glu Gln Leu Thr Val Pro Arg Arg Gly Pro 660 665 670

Asp Glu Gly Ser 675

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2110 844

-12121 PRT

1400> 34

Met Val Gir Lys Ser Arg Ash Gly Gly Val Tyr Pro Gly Pro Ser Gly

- 414. Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro 20 Lt 50
- Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro 35 40 45
- Lys Arg Gly Ser Ile Leu Ser Lys Fro Arg Ala Gly Gly Ala Gly Ala 53 60
- Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe 65 70 75 80
- Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His 35 90 95
- Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe 100 105 110
- Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile 115 120 125
- Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg 130 135 140
- Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg 145 150 155 163
- Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu 165 170 175
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- Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val 210 215 220
- Val Tyr Ala His Ser Lys Slu Leu Val Thr Ala Trp Tyr Ile Gly Phe 225 230 235 240
- Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly 245 250 255
- Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu 260 265 270

The Thr Lea Thr Thr Ile Gly Tyr Sly Asp Lys Tyr Pro Glm Thr Trp 280 Ash Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe 295 300 Fhe Ala Leu Fro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val 310 315 320 Bin Glu Bin His Ard Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala 325 330 335 Ala Gly Leu Ile Glr. Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser 340 345 350 Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr 355 360 365 Val Pro Met Tyr Arg Leu Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu 370 375 380 Arg Asn Leu Lys Ser Lys Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro 385 390 395 400 Pro Glu Pro Ser Fro Ser Gln Lys Val Ser Leu Lys Asp Arg Val Phe 405 410 415 Ser Ser Pro Arg Gly Val Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala 420 425 Gln Thr Val Arg Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser 435 440 Pro Ser Lys Val Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala 455 460 450 Arg Gln Ala Phe Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu 470 475 465 Glu Ala Ser Leu Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro 490 485 Cys Glu Phe Val Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile 505 500 Arg Ala Val Cys Val Met Arg Phe Leu Val Ser Lys Arg Lys Phe Lys

the Ser Lee Ary Pro Tyr Asp Val Met Asp Val lie Glu Gin Tyr Ser 535 Ala Gly His Leu Asp Met Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg 555 563 550 Val Asp Gln lle Val Gly Arg Gly Pro Ala Ile Thr Asp Lys Asp Arg 565 570 573 Thr Lys Gly Pro Ala Glu Ala Glu Leu Pro Glu Asp Pro Ser Met Met 580 585 590 Gly Arg Leu Gly Lys Val Glu Lys Gln Val Leu Ser Met Glu Lys Lys 595 600 605 Leu Asp Phe Leu Val Asn Ile Tyr Met Gln Arg Met Gly Ile Pro Pro 610 615 620 Thr Glu Thr Glu Ala Tyr Phe Gly Ala Lys Glu Pro Glu Pro Ala Pro 625 630 635 640 Pro Tyr His Ser Pro Glu Asp Ser Arg Glu His Val Asp Arg His Gly 645 650 655 Cys Ile Val Lys Ile Val Arg Ser Ser Ser Ser Thr Gly Gln Lys Asn 660 665 670 Phe Ser Ala Pro Pro Ala Ala Pro Pro Val Gln Cys Pro Pro Ser Thr 675 680 685 Ser Trp Gln Pro Gln Ser His Pro Arg Gln Gly His Gly Thr Ser Pro 700 690 695 Val Gly Asp His Gly Ser Leu Val Arg Ile Pro Pro Pro Pro Ala His 705 710 715 Glu Arg Ser Leu Ser Ala Tyr Gly Gly Gly Asn Arg Ala Ser Met Glu 730 725 Phe Leu Arg Gln Glu Asp Thr Pro Gly Cys Arg Pro Pro Glu Gly Thr 740 745 Leu Arg Asp Ser Asp Thr Ser Ile Ser Ile Pro Ser Val Asp His Glu 760

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775

Glu Leu Glu Arg Ser Phe Ser Gly Phe Ser Ile Ser Gln Ser Lys Glu

Ash Led Asp Ala Led Ash Ser Cys Tyr Ala Ala Val Ala Bro Cys Ala 188 - 190 - 198 - 198

Lys Val Arg Pro Tyr Ile Ala Glu Gly Glu Ser Asp Thr Asp Ser Asp 805 810 810

leu Cys Thr Pro Cys Gly Pro Pro Pro Arg Ser Ala Thr Gly Glu Gly 828 830

Fro Phe Gly Asp Val Gly Trp Ala Gly Pro Arg Lys 835 840

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- +12121- PRT
- +213 · Homo sapiens

<:400 - 35

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Asp Gly Gly Gly Gly Gly Gly Ala Ala Asn Pro Ala Gly Gly Asp 20 25 30

Ala Ala Ala Gly Asp Glu Glu Arg Lys Val Gly Leu Ala Pro Gly
35 40 45

Asp Val Glu Gln Val Thr Leu Ala Leu Gly Ala Gly Ala Asp Lys Asp 50 55 60

Sly Thr Leu Leu Glu Gly Gly Gly Arg Asp Glu Gly Gln Arg Arg
65 70 75 80

Thr Pro Gln Gly Ile Gly Leu Leu Ala Lys Thr Pro Leu Ser Arg Pro 85 90 95

Val Lys Arg Asn Asn Ala Lys Tyr Arg Arg Ile Gin Thr Leu Ile Tyr 100 105 110

Asp Ala Leu Glu Arg Pro Arg Gly Trp Ala Leu Leu Tyr His Ala Leu 115 120 125

Val Phe Leu Ile Val Leu Gly Cys Leu Ile Leu Ala Val Leu Thr Thr 130 135 140

Phe Lys Giu Tyr Glu Thr Val Ser Gly Asp Trp Leu Leu Leu Glu

Thr Phe Ala Ilo Phe Ile Phe Gly Ala Glu Phe Ala Leu Arg Ile Trp 185 170 175

Ala Ala Gly Cys Cys Cys Arg Tyr Lys Gly Trp Arg Gly Arg Leu Lys 180 185 190

Phe Ala Arg Lys Pro Leu Cys Met Leu Asp Ile Phe Val Leu Ile Ala 198 200 205

Ser Val Pro Val Val Ala Val Gly Asn Gln Gly Asn Val Leu Ala Thr 210 215 220

Ser Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met Leu Arg Met 225 230 235 240

Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Ala Ile Cys Ala 245 250 255

His Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Fhe Leu Thr Leu 260 265 270

Ile Leu Ser Ser Fhe Leu Val Tyr Leu Val Glu Lys Asp Val Pro Glu 275 280 285

Val Asp Ala Gln Gly Glu Glu Met Lys Glu Slu Fhe Glu Thr Tyr Ala 290 295 300

Asp Ala Leu Trp Trp Gly Leu Ile Thr Leu Ala Thr Ile Gly Tyr Gly 305 310 315 320

Asp Lys Thr Pro Lys Thr Trp Glu Gly Arg Leu Ile Ala Ala Thr Phe 325 330 335

Ser Leu Ile Gly Val Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly 340 345 350

Ser Gly Leu Ala Leu Lys Val Gln Glu Gln His Arg Gln Lys His Phe 355 360 365

Glu Lys Arg Arg Lys Pro Ala Ala Glu Leu Ile 31n Ala Ala Trp Arg 370 375 380

Tyr Tyr Ala Thr Asn Pro Asn Arg Ile Asp Leu Val Ala Thr Trp Arg 385 390 395 400

Phe Tyr Glu Ser Val Val Ser Phe Pro Fhe Phe Arg Lys Glu Gln Leu

Glu Ala Ala Ser Ser Gln Lys Leu Gly Leu Leu Asp Arg Val Arg Leu 425 430

Ser Asn Pro Arg Gly Ser Asn Thr Lys Gly Lys Leu Phe Thr Pro Leu 435

Ash Val Asp Ala Ile Glu Glu Ser Pro Ser Lys Glu Pro Lys Pro Val 450 460

Gly Leu Asn Asn Lys Glu Arg Phe Arg Thr Ala Phe Arg Met Lys Ala 465 470 475 486

Tyr Ala Phe Trp Gln Ser Ser Glu Asp Ala Gly Thr Gly Asp Pro Met 485 490 495

Ala Glu Asp Arg Gly Tyr Gly Asn Asp Phe Pro Ile Glu Asp Met Ile 500 505 510

Fro Thr Leu Lys Ala Ala Ile Arg Ala Val Arg Ile Leu Gln Phe Arg 515 520 525

Leu Tyr Lys Lys Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys 530 535 540

Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Ser Arg 545 550 550

Ile Lys Tyr Leu Gln Thr Arg Ile Asp Met Ile Phe Thr Fro Gly Pro 565 570 575

Fro Ser Thr Pro Lys His Lys Lys Ser Gln Lys Gly Ser Ala Phe Thr 580 585 590

Fhe Pro Ser Gln Gln Ser Pro Arg Asn Glu Pro Tyr Val Ala Arg Pro 595 600 605

Ser Thr Ser Glu Ile Glu Asp Gln Ser Met Met Gly Lys Phe Val Lys 610 615 620

Val Glu Arg Gln Val Gln Asp Met Gly Lys Lys Leu Asp Phe Leu Val 625 630 635 640

Asp Met His Met Gln His Met Glu Arg Leu Gln Val Gln Val Thr Glu 645 650 650

Tyr Tyr Pro Thr Lys Cly Thr Ser Ser Pro Ala Glu Ala Glu Lys Lys

 $e^{i\epsilon_{i}}$

Glu Asp Asr Arg Tyr Ser Asp Leu Lys Thr Ile Ile Cys Asr Tyr Ser 675 680 685

Glu Thr Gly Fro Pro Glu Fro Pro Tyr Ser Phe His Gln Val Thr Ile 690 695 700

Asp Lys Val Ser Pro Tyr Gly Phe Phe Ala His Asp Pro Val Asn Leu 705 715 720

Pro Ary Gly Gly Pro Ser Ser Gly Lys Val Gln Ala Thr Pro Pro Ser 725 730 735

Ser Ala Thr Thr Tyr Val Glu Arg Pro Thr Val Leu Pro Ile Leu Thr 740 750

Leu Leu Asp Ser Arg Val Ser Cys His Ser Gln Ala Asp Leu Gln Gly
755 760 765

Pro Tyr Ser Asp Arg Ile Ser Pro Arg Gln Arg Arg Ser Ile Thr Arg 770 775 780

Asp Ser Asp Thr Pro Leu Ser Leu Met Ser Val Asn His Glu Glu Leu 785 790 795 800

Glu Arg Ser Pro Ser Gly Phe Ser Ile Ser Gln Asp Arg Asp Asp Tyr 805 810 815

Val Phe Gly Pro Ash Gly Gly Ser Ser Trp Met Arg Glu Lys Arg Tyr 820 830

Leu Ala Glu Gly Glu Thr Asp Thr Asp Thr Asp Pro Phe Thr Pro Ser 335 840 845

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H2113-21	
HIZIZH DNA	
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HARRY Pescription of Artificial Sequence: PCR Primer	
Cooling of the circumstate of	
-04000-37	
iggriggdeag getgttgetg g	21
K210 % 38 K211 % 21	
SHILL THE DINA SHIP TO THE SHIP THE SHIP TO THE SHIP T	
<pre>%213% Artificial Sequence</pre>	
-0.20 -	
1227 - Description of Artificial Sequence: PCR Primer	
-:401 + :8	21
grandsgadac etececegtg g	
HILL 7 (1998)	
111 + 1.30	
SIL LL SIMA	
MILIF Artificial Sequence	
+13.2 · +	
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Man Maddaperon of Michigan bodges. Territoria	
-140x + 100	
::st::tycaa tgtagggoot gac	23
-0.10 + 40 -0.11 + 14	
-KUIL-184 -KUIL-180A	
<pre><!-- Substitution</td--><td></td></pre>	
<220%	

August Carrigai no i Arminidial Ceguender 1 % Framer	
rdykrd Inasgyasty sacratatyt ago:	24
<210> 41 <211> 24 <212> DNA <213+ Artificial Sequence	
<2205 k223> Description of Artificial Sequence: PCR Frimer	
<400> 4: pagaagagto aagatgggca ggab	24